REMARKS

Claims 1-11 and 13 have been canceled as the BPAI has affirmed the rejection of these claims. Claim 12 is pending in the instant application. Claim 12 has been rejected and amended to correct informalities in the claim. No new matter has been added by this amendment. Reconsideration is respectfully requested in light of the following remarks.

I. Priority

Applicants are entitled to claim benefit of priority to parent application Serial No. 09/181,601. In response to the Examiner's statement that he cannot determine descriptive support for the NOESY_Assign process, Applicants direct his attention to page 23 (lines 16-32) of the parent application which describes the reasoning constraints in the NOESY_Assign process as corroborated in Example 7, steps 1-12 of Example 8, and Figure 9 of the instant application. In particular, the parent application teaches that spectral overlaps of NOESY spectra are automatically analyzed by using 3D ^{15}N- or ^{13}C-resolved NOESY experiments (page 23, lines 16-17), secondary structure is used to predict NOEs for guiding the analysis of NOESY spectra (page 23, lines 24-28), and a low-resolution structure of the protein obtained in a first pass analysis of the uniquely assigned NOESY cross peaks is used to identify candidate assignments of the remaining unassigned NOESY cross peaks which are inconsistent with the low-resolution structure (page 23, lines 29-32). This constraint reasoning is implemented in the NOESY_Assign process and employed in AUTO_STRUCTURE program as disclosed in the parent application at page 24 (lines 1-16). In this regard, Serial No. 09/181,601

teaches the constraint reasoning implemented in NOESY_Assign as part of an integrated process for gene function discovery and the instant application discloses the NOESY-assign process as one preferred automated NMR data analysis methodology. Therefore, in accordance with MPEP 201.08, Applicants are claiming subject matter that falls within the scope of the disclosure and claims of the parent application and are entitled to claim priority to Serial No. 09/181,601.

II.   Rejection of Claims Under 35 U.S.C. § 102

Claim 12 has been rejected under 35 U.S.C. § 102(b) as being anticipated by the University of Texas at Galveston campus as evidenced by Mumenthaler et al. (*J. Mol. Biol.* (1995) 254:465-480) and an e-mail solicited by the Examiner from Dr. Werner Braun (August 15, 2005). It is suggested that the University of Texas at Galveston campus comprised a computer, an NMR facility which had a spectrometer, data collection device, and computer algorithms to analyze the NMR spectra and determine the tertiary structure of proteins including the NOAH program for automated assignment of NOESY spectra, as well as laboratories for expressing proteins, access to the Wisconsin programs which can parse target polynucleotides, and internet access to the Protein Data Bank and the DALI web server. It is suggested that the elements of the claim not found in Mumenthaler are met by the e-mail from Dr. Braun. The Examiner suggests that Dr. Braun notes that UTMB had a laboratory that could express proteins in 1995, internet access to the protein databank at Brookhaven National Laboratory, and a computer algorithm capable of determining 3D structural homology between the known and unknown proteins as

discussed in his e-mail. Applicants respectfully traverse this rejection.

The BPAI stated that "an anticipation rejection must be based on substantive evidence, not speculation" and required that the Examiner point out *in Mumenthaler et al.* teachings pertaining to a laboratory for expressing protein domains, a database which stores the structure and function of known proteins, and a computer capable of determining the structure of an unknown protein and a known protein. The e-mail by Dr. Braun does not constitute such "substantive evidence" of the existence of these elements in Mumenthaler et al. Accordingly, Mumenthaler et al. does not anticipate the claimed invention.

As indicated by the BPAI, Mumenthaler et al. fail to teach a lab for expressing the putative domain of an unknown protein, a database, and a fourth computer. In this regard, the e-mail by Dr. Braun merely makes note of the existence of these missing elements <u>somewhere</u> on the University of Texas at Galveston campus or at Brookhaven National Laboratory. Further, Mumenthaler et al. fail to teach automated NMR resonance assignments and NOESY_Assign. In contrast, step F teaches a computer program for automating individual spin resonances to individual amino acids of a polypeptide and step I teaches NOESY_Assign as a preferred methodology for determining the tertiary structure of a polypeptide of unknown function for 3D structure homology analysis. To clarify these distinctions, Applicants have amended claim 12 in accordance with the disclosure at page 23 (line 22) to page 24 (line 14) and Examples 7 and 8. Moreover, nowhere in the teachings of Mumenthaler et al. are all the essential elements of the claim combined in an *integrated* system for

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deducing gene function from 3D structural analysis. In contrast, the instant claim specifies that the elements are *integrated*. In the context of the present invention such integration is achieved by equipping a

> "dedicated laboratory staffed with artisans skilled in relevant arts (e.g., NMR and X-Ray crystallography, molecular biology, biochemistry, etc.). Preferably, such a laboratory is further equipped with state of the art equipment for the sequencing, sub-cloning, expression, purification, screening and analysis of the protein domains of interest. The rate limiting component of this high-throughput "engine" is the number of NMR machines within the laboratory. Thus, the rate at which protein domains can be characterized will increase with the addition of additional NMR machines. Unlike conventional methodology, the present invention provides a method for determining the 3D structure of unknown protein domains whose rate is not solely dependent on the number of artisans skilled in 3D protein structure determination."

See page 27, lines 20-31, of the specification under the heading "Integration Into A Large-Scale, High-Throughput "Engine" For Structural And Functional Analysis Of Hundreds Of Human Genes". It is quite clear from this passage that the mere existence of each element somewhere on a University campus or the Internet by no means constitutes an integrated system for deducing gene function from 3D structure.

Further, Dr. Braun's e-mail merely states that "UTMB had already a protein expression lab in place, directed by Dr. T. Wood, when I joined UTMB in the fall of 1995." Dr. Wood is not a co-author of Mumenthaler et al. and the presence of Dr. Wood's lab at UTMB is apparently independent of Dr. Braun's laboratory and research effort, by his own admission. Further, Dr. Braun merely states he had "access" to a databank at Brookhaven National Laboratory. There is no indication he utilized it in

Mumenthaler et al. Not only are the deficiencies of Mumenthaler et al. pointed out by the BPAI unmet by this e-mail, the Examiner's representation of Dr. Braun's statements are inaccurate and frankly misleading.

In so far as the e-mail by Dr. Braun cannot be reasonably considered substantive evidence that Mumenthaler et al. had access to or ever used such an integrated system, and the fact that Mumenthaler et al. fail to teach each and every element of the claim (as explicitly pointed out by the BPAI), the instant invention is not anticipated in accordance with the requirements set forth under 35 U.S.C. § 102(b). Withdrawal of this rejection is therefore respectfully requested.
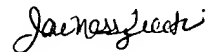
III. Conclusion

The Applicants believe that the foregoing comprises a full and complete response to the Office Action of record.

Accordingly, favorable reconsideration and subsequent allowance of the pending claims is earnestly solicited.

Respectfully submitted,

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